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SEQUENCE LISTING

5		(i)	APPLICANT:	Helgeson,	John	Ρ.
	•			Austin, Sa	andra	
				Naess, San	ca K.	

- (ii) TITLE OF THE INVENTION: GERMPLASM AND MOLECULAR 10 MARKERS FOR DISEASE RESISTANCE IN POTATO
 - (iii) NUMBER OF SEQUENCES: 5
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Dann, Dorfman, Herrell & Skillman
 - (B) STREET: 1601 Market Street, Suite 720
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
- (F) ZIP: 19103 20
 - (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not yet assigned
 - (B) FILING DATE: 27-JUL-1998
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/054,267
 - (B) FILING DATE: 30-JUL-1997
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Janet E. Reed
 - (B) REGISTRATION NUMBER: 36,252
 - (C) REFERENCE/DOCKET NUMBER: P98003WO
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 215-563-4100
 - (B) TELEFAX: 215-563-4044
- 45 (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 586 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
- 55 (iv) ANTISENSE: NO
 - (V) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE: Solanum bulbocastanum



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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
5	GGCACTGAGG GGTAGTAAGC CTCCTGCATG TACTAAGTAT GGTAGATCCA CTCAGGGTTG TGCCATGATG GCTTAACTGG TTGTTTCAAG TATGGCCAGA ACGGTTATTT TATGAGAGAG TTTCCAAAGA ACATGCAGGG TAATGGTAAT GGGGATAATA GAACCCAGTC TTCTTCAGTG ACTCCACCAG ACAGAGCTGC ATCTAGAGGA GCTACTTCGA GGCAGGCGGA GGATCGAACG TCTTTATGCT ATCACTAGTC GCCAAGAGAA AGAGGATTCG CCAGATGTTG TCACTGGTAT GATCCAAGTC TTTAACTTTG ATTTTATACT TTTCTAGATC CAGGAGCGAG TTTATCCTTT GTAACTCCTT ATGTTGCGGT TAATTTTGAT GTTCTTCCTA AGAAACTTAT TGAGCCCTTC AGTGTTTCTA CACTTGTTGG TCTATTATAG TAGAGAGAGT CTGTTATGAT TGTACCGTTT TCGTCAATCA CAAGAGCACC ATGGTTGATT TAGTTGAGTT AGACATGGTA GAATTTGATG	420
	TTATTCTTGG TATGGACTGA CTTCATTCTT GTTATGCCTC AGTGCC	586
15	(2) INFORMATION FOR SEQ ID NO:2:(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 587 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: cDNA(iii) HYPOTHETICAL: NO(iv) ANTISENSE: NO(v) FRAGMENT TYPE:(vi) ORIGINAL SOURCE: Solanum bulbocastanum	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
30	GTGGTCCGCA TATAACTCAA GAACTTGTAA TGCATGTATC GGATATATGT ATACATGTTG TCTTTTGCAA AGTTTACTTT TTTATTANTT AATCTTGTTT GTGTCTGGAG GTGGTGGTGG GGTGGGATAG TGGTGAAGCT AGAAATTTAG TTAAGTGTGT TCAAGATTTA AATATACATA TGAAAAATAA TTTTTGATCT ATATATATAG TTATAATTTT NTGATGAAGG TAGTTCAACT GACCACCGT NACTACATGT GGCTACCGTA CTGGGTGGG TGGAAGGTCN TGGTGTTTAC	60 120 180 240 300
35	AGTGATGTGG GGGCCTCTGA AATGCTTTTG TGGGCAATGT GGGAATTACT GTTTATCTTT TCTTTATTGA AGTCATTGAG TGTTTGAGTT ATTTAACTAT GAAAGGTAGC TAGTGGGTAA TGTTATTGAT GACTTTGTGT GAAGAACAAA ATGTCAATCA TTCAGAGCGT TCAATGGGGG CACGTGCTGG AGTCCCATTT GGATTATTGG GTTTAGGGGT TGCCTAGGTG GTGGTGGTGG TGGTTGGTAA TGGATAATAA TGTTGGTGAA ATATGGGTGC GGAGGAG	360 420 480
40	(2) INFORMATION FOR SEQ ID NO:3:	
45	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 596 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
50	<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: tomato</pre>	

55	(xi) SEQUENCI	E DESCRIP	TION:	SEQ	ID	ИО:3:	
	GTTGGGCAGA	ACACCTAGGA	ACDG 4TD 4D4	тстсььс	ጥር አ	ጥእርጥ	יייירכזירכ	_

	GTTGGGCAGA						60
	ATAGTTGTAG	ACAACCCGTG	AATCTCAGGA	GACAAAATGA	TGTTTGCCCC	AATTGCGGTG	120
	GTGGATTTGT	TCAAGAGCTT	GAAGACATAA	CGAGTAGTAG	TGTAGATAAT	CAGACCCAGA	180
60	GGCCGAGATT	CATGGAATCC	GTCTCAAACT	TTTTAAGACG	ACAAATCTCA	GCTACAAGTA	240
	ATACTTCTGA	GAGAGGGAGA	TCTGATGGGG	GTGCTGAACG	AGGAAATTTG	TGGAATCCGT	300



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5	TGCTGATTTT CAGTGGTGAT ACGCCTGTTC ATATGCCTGG GGATGGTGGA GTTTTGGAGT TTCTTAATGA GGCACCTTGG ATTCCGAGCA AGAAAATGGT GGTGATTATT TTGTTGGTCC AGGAGTGGAG GAATTTTTTG AAGAAATTGT AAATAGAAAT CAGCGTGGTG CTCCTCCC TGTCTCGAGA TGTTCAATTG ATTCCCTACC AACAGTCAAG ATATCAAAAA AGGATGTTAG ATCGGATTCG CACTGCCCTG TTTGTAAGGA GAAATTTGCT CTGGGGACTA AGGCAA	360 420 480 540 596
	(2) INFORMATION FOR SEQ ID NO:4:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 589 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
15	<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE:</pre>	
	(v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: Solanum tuberosum	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
25	GTTGGGCAGA AGAGCTAGGA AGAGTAAGCA TGTCAAGTGA CAGTTGCAGC CACTGGTGTT ATAGTTGTAG ACAACCCGTG AATCTCAGGA GACAAAATGA TGTTTGCCCC AATTGCAGTG GTGGATTTGT TCAAGAGCTT GAAGACATAA CGAGTAGTAG TGTAGATAAT CAGAGCCAGA GGCCGAGATT TATGGAATCC GTCTCAAACT TTTTAAGACG ACAAATCGCT ACAAGTAATA CTTCTGAGAG AGGGAGATCT GATGGGGGTG CTGAACGAGG AAATTTATGG AATCCATTGC TGATTTTCAG TGGTGATACG CCTGTTCAAG ATGCCTGGGG ATGGTGGAGT TTTTGGAGTTT	60 120 180 240 300 360
30	CTTAATGAGG CTCTTGGCTT CCGACAAGAA AATGGTGGTG ATTATTTTGT TGGTCCAGGA GTGGAGGAAT TTTTTGAAGA AATTGTAAAT AGAAATCAGC GTGGTGCTCC TCCTGCCTCA AGATGTTCAA TTGATTCCCT ACCAACAGTC AAGATATCGA AAAAAGATGT TAGATCGGAT TCTCACTGCC CTGTTTGTAA AGAGAAATTT GCTCTGGGGA CTAAGGCAA	420 480 540 589
	(2) INFORMATION FOR SEQ ID NO:5:	
35	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 592 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	 (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: Solanum bulbocastanum 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
50	GTTGGGCAGA AGAGCTAGGA AGAGTAAGCA TGTCAAGTGA CAGTTGCAGC CACTGGTGTT ATAGTTGTAG ACAACCCGTG AATCTCAGCA GACAAAATGA TGTTTGCCCC AATTGCGGTG GTGGATTTGT TCAAGAGCTT GAAGACATAA CGAGTAGTAG TGTAGATAAT CAGAGCCAGA	60 120 180
	GGCCGAGATT CATGGAATCC GTCTCAAACT TTTTAAGACG ACAAATCCCA ACTACAAGTA	240
55	ATACTTCTTG AGAGAGGAG ATCTGATGGG GGTGCTGAAC GAGGAAATTT GTGGAATCCG TTGCTGATTT TCAGTGGTGA TACACCTGTT CGGATGCCTG GGGATGGTGG AGTTTTGGAG TTTCTTAATG AGGCTCTTGG CTTTCGACAA GAAAATGGTG GTGANTATTT TGTTGGCCCA GGAGTGGAGG AGTTTTTTGA AGAAATTGTA AATAAAAATC AGCGTGGTGC TCCTCCTGTC TCAAGATGCT CAATTGATTC CCTACCAACA GTCAAGATAT CGAAAAAGGA TGTTAGATCG GATTCTCACT GCCCTGTTTG TAAAGAGAAA TTTGCTCTGG GGACTAAGGC AA	300 360 420 480 540 592